

281642US0XPCT.ST25
SEQUENCE LISTING

<110> Patek, Miroslav
Elisakova, Veronika

<120> FEEDBACK RESISTANT ACETOHYDROXY ACID SYNTHETHASE MUTANTS

<130> 281642US0XPCT

<140> US 10/561,906
<141> 2005-12-21

<150> PCT/EP04/06157
<151> 2004-06-08

<150> EP 03014640.1
<151> 2003-06-26

<160> 12

<170> PatentIn version 3.3

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

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1 5 10 15	
gac gta gac gat gac ttt tcc cgc gta tca ggt atg ttc acc cga cgc	96
Asp Val Asp Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg	
20 25 30	
gca ttc aac ctc gtg tcc ctc gtg tct gca aag acc gaa aca cac ggc	144
Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly	
35 40 45	
atc aac cgc atc acg gtt gtc gac gcc gac gag ctc aac att gag	192
Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu	
50 55 60	
cag atc aac aag cag ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg	240
Gln Ile Asn Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val	
65 70 75 80	
cga ctt gat gaa gag acc act atc gcc cgc gca atc atg ctg gtt aag	288
Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys	
85 90 95	
gtc tct gcg gac agc acc aac cgt ccg cag atc gtc gac gcc gcg aac	336
Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn	
100 105 110	
atc ttc cgc gcc cga gtc gtc gac gtg gct cca gac tct gtg gtt att	384
Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile	
115 120 125	

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gaa tcc aca ggc acc cca ggc aag ctc cgc gca ctg ctt gac gtq atg	432
Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met	
130 135 140	
gaa caa ttc gaa atc cgc gaa ctg atc caa tcc gga cag att gca ctc	480
Glu Gln Phe Glu Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu	
145 150 155 160	
aac cgc ggt ccg aag acc atg gct ccg gcc aag atc taa	519
Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile	
165 170	
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Asp Val Asp Asp Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg	
20 25 30	
Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly	
35 40 45	
Ile Asn Arg Ile Thr Val Val Asp Ala Asp Glu Leu Asn Ile Glu	
50 55 60	
Gln Ile Asn Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val	
65 70 75 80	
Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys	
85 90 95	
Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn	
100 105 110	
Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile	
115 120 125	
Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met	
130 135 140	
Glu Gln Phe Glu Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu	
145 150 155 160	
Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile	
165 170	

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<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

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1				5				10					15			
gac	gta	gac	ggt	gac	ttt	tcc	cgc	gta	tca	ggt	atg	ttc	acc	cga	cgc	
Asp	Val	Asp	Gly	Asp	Phe	Ser	Arg	Val	Ser	Gly	Met	Phe	Thr	Arg	Arg	
			20					25					30			
gca	ttc	aac	ctc	gtg	tcc	ctc	gtg	tct	gca	aag	acc	gaa	aca	cac	ggc	
Ala	Phe	Asn	Leu	Val	Ser	Leu	Val	Ser	Ala	Lys	Thr	Glu	Thr	His	Gly	
			35					40				45				
atc	aac	cgc	atc	acg	gtt	gtt	gtc	gac	gcc	gac	gag	ctc	aac	att	gag	
Ile	Asn	Arg	Ile	Thr	Val	Val	Val	Asp	Ala	Asp	Glu	Leu	Asn	Ile	Glu	
			50					55			60					
cag	atc	acc	aag	cag	ctc	aac	aag	ctg	atc	ccc	gtg	ctc	aaa	gtc	gtg	
Gln	Ile	Thr	Lys	Gln	Leu	Asn	Lys	Leu	Ile	Pro	Val	Leu	Lys	Val	Val	
			65					70			75			80		
cga	ctt	gat	gaa	gag	acc	act	atc	gcc	cgc	gca	atc	atg	ctg	gtt	aag	
Arg	Leu	Asp	Glu	Glu	Thr	Thr	Ile	Ala	Arg	Ala	Ile	Met	Leu	Val	Lys	
			85					90					95			
gtc	tct	gcg	gac	agc	acc	aac	cgt	ccg	cag	atc	gtc	gac	gcc	gcg	aac	
Val	Ser	Ala	Asp	Ser	Thr	Asn	Arg	Pro	Gln	Ile	Val	Asp	Ala	Ala	Asn	
			100					105					110			
atc	ttc	cgc	gcc	cga	gtc	gtc	gac	gtg	gct	cca	gac	tct	gtg	gtt	att	
Ile	Phe	Arg	Ala	Arg	Val	Val	Asp	Val	Ala	Pro	Asp	Ser	Val	Val	Ile	
			115					120				125				
gaa	tcc	aca	ggc	acc	cca	ggc	aag	ctc	cgc	gca	ctg	ctt	gac	gtg	atg	
Glu	Ser	Thr	Gly	Thr	Pro	Gly	Lys	Leu	Arg	Ala	Leu	Leu	Asp	Val	Met	
			130					135			140					
gaa	cca	tcc	gga	atc	gcg	gaa	ctg	atc	caa	tcc	gga	cag	att	gca	ctc	
Glu	Pro	Ser	Gly	Ile	Ala	Glu	Leu	Ile	Gln	Ser	Gly	Gln	Ile	Ala	Leu	
			145					150			155			160		
aac	cgc	ggt	ccg	aag	acc	atg	gct	ccg	gcc	aag	atc	taa				519
Asn	Arg	Gly	Pro	Lys	Thr	Met	Ala	Pro	Ala	Lys	Ile					
			165					170								

<210> 4
<211> 172
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<400> 4

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Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
1 5 10 15

Asp Val Asp Gly Asp Phe Ser Arg Val Ser Gly Met Phe Thr Arg Arg
20 25 30

Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu
50 55 60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val
65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys
85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn
100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met
130 135 140

Glu Pro Ser Gly Ile Ala Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu
145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile
165 170

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caatcagatt aattgctgtt ta

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Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
 1 5 10 15

Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg
 20 25 30

Ala Phe Asn Leu Val Ser Leu Val Ser Ala Lys Thr Glu Thr His Gly
 35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp
 50 55

<210> 11
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 <212> PRT
 <213> S. cinnamonensis

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Met Ser Thr Lys His Thr Leu Ser Val Leu Val Glu Asn Lys Pro Gly
 1 5 10 15

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Val Leu Ala Arg Ile Thr Ala Leu Phe Ser Arg Arg Gly Phe Asn Ile
20 25 30

Asp Ser Leu Ala Val Gly Val Thr Glu His Pro Asp Ile Ser Arg Ile
35 40 45

Thr Ile Val Val Asn
50

<210> 12
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<212> PRT
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<400> 12

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Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
20 25 30

Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
35 40 45

Lys Ser His Ile Trp Leu Leu Val Asn
50 55